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4 NOV 09 2001
TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/991,143ADATE: 10/29/2001
TIME: 14:57:08Input Set : A:\08-991143 Sequence Listing.txt
Output Set: N:\CRF3\10292001\H991143A.raw# 3
Raw Seq
Kashy

4 <110> APPLICANT: Conti-Fine, B.
 6 <120> TITLE OF INVENTION: Methods to treat undesirable immune responses
 8 <130> FILE REFERENCE: 600.423US1
 10 <140> CURRENT APPLICATION NUMBER: US 08/991,143A
 11 <141> CURRENT FILING DATE: 1997-12-16
 13 <160> NUMBER OF SEQ ID NOS: 3
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1667
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <400> SEQUENCE: 1

ENTERED

| | |
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| 23 aagcacaggc caccactctg ccttggtcca cacaagctcc ggtagcccat ggagccctgg | 60 |
| 24 cctctcctcc tgctcttttag cctttgctca gctggcctcg tcttgggctc cgaacatgag | 120 |
| 25 acccgtcttg tggcaaagct atttaaagac tacagcagcg tgggtgcggcc agtgggaagac | 180 |
| 26 caccgccagg tcgtggaggt caccgtgggc ctgcagctga tacagctcat caatgtggat | 240 |
| 27 gaagtaaadc agatcgtgac aaccaatgtg cgtctgaaac agcaatgggt ggattacaac | 300 |
| 28 ctaaaatgga atccagatga ctatggcggg gtgaaaaaaa ttcacattcc ttcagaaaag | 360 |
| 29 atctggcgcc cagacctgtg tctctataac aatgcagatg gtgactttgc tattgtcaag | 420 |
| 30 ttcaccaaag tgctcctgca gtacactggc cacatcacgt ggacacctcc agccatcttt | 480 |
| 31 aaaagctact gtgagatcat cgtcacccac tttccctttg atgaacagaa ctgcagcatg | 540 |
| 32 aagctgggca cctggacctc cgacggctct gtcgtggcca tcaacctcga aagcgaccag | 600 |
| 33 ccagacctga gcaacttcat ggagagcggg gagtgggtga tcaaggagtc ccggggctgg | 660 |
| 34 aagcactccg tgacctattc ctgctgcccc gacacccctt acctggacat cacctaccac | 720 |
| 35 ttctctatgc agcgccctgcc cctctacttc atcgtaacg tcatcatccc ctgcctgctc | 780 |
| 36 ttctccttct taactggcct ggtattctac ctgcccacag actcagggga gaagatgact | 840 |
| 37 ctgagcatct ctgtcttact gtctttgact gtgttccttc tggtcacgtg ggagctgac | 900 |
| 38 cctccacgt ccagtgcgtg gcccttgatt gaaaaataca tgctgttcac catggtgttc | 960 |
| 39 gtcattgcct ccatcatcat cactgtcatc gtcatcaaca cacaccaccg ctacccaccg | 1020 |
| 40 acccatgtca tgcccaactg ggtgcggaag gtttttatcg acactatccc aaatatcatg | 1080 |
| 41 ttttttccca caatgaaaag accatccaga gaaaagcaag acaaaaagat ttttacagaa | 1140 |
| 42 gacattgata tctctgacat ttctggaaag ccagggcctc caccatggg cttccactct | 1200 |
| 43 cccctgatca aacaccccca ggtgaaaagt gccatcgagg gcatcaagta catcgagag | 1260 |
| 44 accatgaagt cagaccagga gtctaacaat gcggcggcag agtgggaagta cgttgcaatg | 1320 |
| 45 gtgatggacc acatactcct cggagctctc atgcttggtt gcatcatcgg aaccctagcc | 1380 |
| 46 gtgtttgcag gtcgactcat tgaattaaat cagcaaggat gagcagaaaa tgagctgagc | 1440 |
| 47 ttagctctgc cctggaacct accagagcag agaaggcgag gagaggaaga tttgtctact | 1500 |
| 48 tgctccactc gcacttatca aacgtgttat attccatact tattattgat gataagattt | 1560 |
| 49 acctttatgt aagtttatgg ccttgaagtg ttttcatatt gcttctccct ttagttctgc | 1620 |
| 50 tgtctccctg aagagtgaac cctcttttagt aaatgaaact aatcact | 1667 |

53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 457
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Homo sapiens
 58 <400> SEQUENCE: 2
 59 Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala Gly
 60 1 5 10 15

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61 Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe
62          20          25          30
63 Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val
64          35          40          45
65 Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp
66          50          55          60
67 Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp
68 65          70          75          80
69 Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys
70          85          90          95
71 Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu
72          100          105          110
73 Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val
74          115          120          125
75 Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe
76          130          135          140
77 Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln
78 145          150          155          160
79 Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val
80          165          170          175
81 Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
82          180          185          190
83 Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val
84          195          200          205
85 Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His
86          210          215          220
87 Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile
88 225          230          235          240
89 Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro
90          245          250          255
91 Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser
92          260          265          270
93 Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser
94          275          280          285
95 Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe
96          290          295          300
97 Val Ile Ala Ser Ile Ile Ile Thr Val Ile Val Ile Asn Thr His His
98 305          310          315          320
99 Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe
100          325          330          335
101 Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro
102          340          345          350
103 Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile
104          355          360          365
105 Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser
106          370          375          380
107 Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys
108 385          390          395          400
109 Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala

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110                               405                               410.                               415
111 Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly
112                               420                               425                               430
113 Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
114                               435                               440                               445
115 Arg Leu Ile Glu Leu Asn Gln Gln Gly
116                               450                               455
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 437
121 <212> TYPE: PRT
122 <213> ORGANISM: Torpedo californica
124 <400> SEQUENCE: 3
125 Ser Glu His Glu Thr Arg Leu Val Ala Asn Leu Leu Glu Asn Tyr Asn
126 1                               5                               10                               15
127 Lys Val Ile Arg Pro Val Glu His His Thr His Phe Val Asp Ile Thr
128                               20                               25                               30
129 Val Gly Leu Gln Leu Ile Gln Leu Ile Ser Val Asp Glu Val Asn Gln
130                               35                               40                               45
131 Ile Val Glu Thr Asn Val Arg Leu Arg Gln Gln Trp Ile Asp Val Arg
132 50                               55                               60
133 Leu Arg Trp Asn Pro Ala Asp Tyr Gly Gly Ile Lys Lys Ile Arg Leu
134 65                               70                               75                               80
135 Pro Ser Asp Asp Val Trp Leu Pro Asp Leu Val Leu Tyr Asn Asn Ala
136                               85                               90                               95
137 Asp Gly Asp Phe Ala Ile Val His Met Thr Lys Leu Leu Leu Asp Tyr
138                               100                               105                               110
139 Thr Gly Lys Ile Met Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys
140                               115                               120                               125
141 Glu Ile Ile Val Thr His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met
142                               130                               135                               140
143 Lys Leu Gly Ile Trp Thr Tyr Asp Gly Thr Lys Val Ser Ile Ser Pro
144 145                               150                               155                               160
145 Glu Ser Asp Arg Pro Asp Leu Ser Thr Phe Met Glu Ser Gly Glu Trp
146                               165                               170                               175
147 Val Met Lys Asp Tyr Arg Gly Trp Lys His Trp Val Tyr Tyr Thr Cys
148                               180                               185                               190
149 Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His Phe Ile Met Gln
150                               195                               200                               205
151 Arg Ile Pro Leu Tyr Phe Val Val Asn Val Ile Ile Pro Cys Leu Leu
152                               210                               215                               220
153 Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro Thr Asp Ser Gly
154 225                               230                               235                               240
155 Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser Leu Thr Val Phe
156                               245                               250                               255
157 Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser Ser Ala Val Pro
158                               260                               265                               270
159 Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Ile Phe Val Ile Ser Ser
160                               275                               280                               285
161 Ile Ile Ile Thr Val Val Val Ile Asn Thr His His Arg Ser Pro Ser

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162      290      295      300
163 Thr His Thr Met Pro Gln Trp Val Arg Lys Ile Phe Ile Asp Thr Ile
164 305      310      315      320
165 Pro Asn Val Met Phe Phe Ser Thr Met Lys Arg Ala Ser Lys Glu Lys
166      325      330      335
167 Gln Glu Asn Lys Ile Phe Ala Asp Asp Ile Asp Ile Ser Asp Ile Ser
168      340      345      350
169 Gly Lys Gln Val Thr Gly Glu Val Ile Phe Gln Thr Pro Leu Ile Lys
170      355      360      365
171 Asn Pro Asp Val Lys Ser Ala Ile Glu Gly Val Lys Tyr Ile Ala Glu
172      370      375      380
173 His Met Lys Ser Asp Glu Glu Ser Ser Asn Ala Ala Glu Glu Trp Lys
174 385      390      395      400
175 Tyr Val Ala Met Val Ile Asp His Ile Leu Leu Cys Val Phe Met Leu
176      405      410      415
177 Ile Cys Ile Ile Gly Thr Val Ser Val Phe Ala Gly Arg Leu Ile Glu
178      420      425      430
179 Leu Ser Gln Glu Gly
180      435

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VERIFICATION SUMMARY

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